

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/637,614

DATE: 07/26/2001
TIME: 09:58:44

Input Set : N:\Crf3\RULE60\09637614.txt
Output Set: N:\CRF3\07262001\I637614.raw

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: Koieda, Shohei
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
11 (iii) NUMBER OF SEQUENCES: 118
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
15 (B) STREET: 121 South Eighth Street, Ste. 1600
16 (C) CITY: Minneapolis
17 (D) STATE: MN
18 (E) COUNTRY: USA
19 (F) ZIP: 55402

(v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ Version 2.0b

(vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/637,614
C--> 29 (B) FILING DATE: 11-Aug-2000

(vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 09/096,749
33 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Ann S. Viksnins
37 (B) REGISTRATION NUMBER: 37,748
38 (C) REFERENCE/DOCKET NUMBER: 109.034US1

(ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: (612) 373-6900
42 (B) TELEFAX: (612) 339-3061

45 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 14 amino acids
49 (B) TYPE: amino acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

C--> 55 (iv) ANTI-SENSE: NO

56 (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

61 Ala Arg Glu Arg Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly
62 1 5 10

64 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

67 (A) LENGTH: 17 amino acids

ENTERED

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68          (B) TYPE: amino acid
69          (C) STRANDEDNESS: single
70          (D) TOPOLOGY: linear
72      (ii) MOLECULE TYPE: peptide
73      (iii) HYPOTHETICAL: NO
C--> 74      (iv) ANTI-SENSE: NO
75          (v) FRAGMENT TYPE: internal
76          (vi) ORIGINAL SOURCE:
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80  Ala Arg Gly Ala Val Val Ser Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
81    1             5             10             15
82  Gly
85 (2) INFORMATION FOR SEQ ID NO: 3:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 16 amino acids
89          (B) TYPE: amino acid
90          (C) STRANDEDNESS: single
91          (D) TOPOLOGY: linear
93      (ii) MOLECULE TYPE: peptide
94      (iii) HYPOTHETICAL: NO
C--> 95      (iv) ANTI-SENSE: NO
96          (v) FRAGMENT TYPE: internal
97          (vi) ORIGINAL SOURCE:
99      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
101 Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile
102  1             5             10             15
104 (2) INFORMATION FOR SEQ ID NO: 4:
106      (i) SEQUENCE CHARACTERISTICS:
107          (A) LENGTH: 12 amino acids
108          (B) TYPE: amino acid
109          (C) STRANDEDNESS: single
110          (D) TOPOLOGY: linear
112      (ii) MOLECULE TYPE: peptide
113      (iii) HYPOTHETICAL: NO
C--> 114      (iv) ANTI-SENSE: NO
115          (v) FRAGMENT TYPE: internal
116          (vi) ORIGINAL SOURCE:
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
120 Tyr Ala Glu Arg Asp Tyr Arg Leu Asp Tyr Pro Ile
121  1             5             10
123 (2) INFORMATION FOR SEQ ID NO: 5:
125      (i) SEQUENCE CHARACTERISTICS:
126          (A) LENGTH: 12 amino acids
127          (B) TYPE: amino acid
128          (C) STRANDEDNESS: single
129          (D) TOPOLOGY: linear
131      (ii) MOLECULE TYPE: peptide
132      (iii) HYPOTHETICAL: NO
C--> 133      (iv) ANTI-SENSE: NO

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```

134      (v) FRAGMENT TYPE: internal
135      (vi) ORIGINAL SOURCE:
137      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
139  Tyr Ala Val Arg Asp Tyr Arg Leu Asp Tyr Pro Ile
140    1          5          10
142 (2) INFORMATION FOR SEQ ID NO: 6:
144      (i) SEQUENCE CHARACTERISTICS:
145          (A) LENGTH: 16 amino acids
146          (B) TYPE: amino acid
147          (C) STRANDEDNESS: single
148          (D) TOPOLOGY: linear
150      (ii) MOLECULE TYPE: peptide
151      (iii) HYPOTHETICAL: NO
C--> 152      (iv) ANTI-SENSE: NO
153      (v) FRAGMENT TYPE: internal
154      (vi) ORIGINAL SOURCE:
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
158  Tyr Ala Val Arg Asp Tyr Arg Leu Asp Tyr Ala Ser Ser Lys Pro Ile
159    1          5          10          15
161 (2) INFORMATION FOR SEQ ID NO: 7:
163      (i) SEQUENCE CHARACTERISTICS:
164          (A) LENGTH: 13 amino acids
165          (B) TYPE: amino acid
166          (C) STRANDEDNESS: single
167          (D) TOPOLOGY: linear
169      (ii) MOLECULE TYPE: peptide
170      (iii) HYPOTHETICAL: NO
C--> 171      (iv) ANTI-SENSE: NO
172      (v) FRAGMENT TYPE: internal
173      (vi) ORIGINAL SOURCE:
175      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
177  Tyr Ala Val Arg Asp Tyr Arg Leu Asp Tyr Lys Pro Ile
178    1          5          10
180 (2) INFORMATION FOR SEQ ID NO: 8:
182      (i) SEQUENCE CHARACTERISTICS:
183          (A) LENGTH: 11 amino acids
184          (B) TYPE: amino acid
185          (C) STRANDEDNESS: single
186          (D) TOPOLOGY: linear
188      (ii) MOLECULE TYPE: peptide
189      (iii) HYPOTHETICAL: NO
C--> 190      (iv) ANTI-SENSE: NO
191      (v) FRAGMENT TYPE: internal
192      (vi) ORIGINAL SOURCE:
194      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
196  Tyr Ala Val Arg Asp Tyr Arg Ser Lys Pro Ile
197    1          5          10
199 (2) INFORMATION FOR SEQ ID NO: 9:
201      (i) SEQUENCE CHARACTERISTICS:

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```

202      (A) LENGTH: 14 amino acids
203      (B) TYPE: amino acid
204      (C) STRANDEDNESS: single
205      (D) TOPOLOGY: linear
207      (ii) MOLECULE TYPE: peptide
208      (iii) HYPOTHETICAL: NO
C--> 209      (iv) ANTI-SENSE: NO
210      (v) FRAGMENT TYPE: internal
211      (vi) ORIGINAL SOURCE:
213      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
215 Tyr Ala Val Thr Arg Asp Tyr Arg Leu Ser Ser Lys Pro Ile
216   1             5             10
218 (2) INFORMATION FOR SEQ ID NO: 10:
220      (i) SEQUENCE CHARACTERISTICS:
221          (A) LENGTH: 15 amino acids
222          (B) TYPE: amino acid
223          (C) STRANDEDNESS: single
224          (D) TOPOLOGY: linear
226      (ii) MOLECULE TYPE: peptide
227      (iii) HYPOTHETICAL: NO
C--> 228      (iv) ANTI-SENSE: NO
229      (v) FRAGMENT TYPE: internal
230      (vi) ORIGINAL SOURCE:
232      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
234 Tyr Ala Val Thr Glu Arg Asp Tyr Arg Leu Ser Ser Lys Pro Ile
235   1             5             10             15
237 (2) INFORMATION FOR SEQ ID NO: 11:
239      (i) SEQUENCE CHARACTERISTICS:
240          (A) LENGTH: 15 amino acids
241          (B) TYPE: amino acid
242          (C) STRANDEDNESS: single
243          (D) TOPOLOGY: linear
245      (ii) MOLECULE TYPE: peptide
246      (iii) HYPOTHETICAL: NO
C--> 247      (iv) ANTI-SENSE: NO
248      (v) FRAGMENT TYPE: internal
249      (vi) ORIGINAL SOURCE:
251      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
253 Tyr Ala Val Ala Val Ser Tyr Tyr Ala Met Asp Tyr Pro Ile
254   1             5             10             15
256 (2) INFORMATION FOR SEQ ID NO: 12:
258      (i) SEQUENCE CHARACTERISTICS:
259          (A) LENGTH: 16 amino acids
260          (B) TYPE: amino acid
261          (C) STRANDEDNESS: single
262          (D) TOPOLOGY: linear
264      (ii) MOLECULE TYPE: peptide
265      (iii) HYPOTHETICAL: NO
C--> 266      (iv) ANTI-SENSE: NO

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```

267      (v) FRAGMENT TYPE: internal
268      (vi) ORIGINAL SOURCE:
270      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
272 Tyr Ala Val Thr Ala Val Val Ser Tyr Tyr Ala Ser Ser Lys Pro Ile
273  1          5          10          15
275 (2) INFORMATION FOR SEQ ID NO: 13:
277      (i) SEQUENCE CHARACTERISTICS:
278          (A) LENGTH: 59 base pairs
279          (B) TYPE: nucleic acid
280          (C) STRANDEDNESS: single
281          (D) TOPOLOGY: linear
283      (ii) MOLECULE TYPE: cDNA
284      (iii) HYPOTHETICAL: NO
C--> 285      (iv) ANTI-SENSE: NO
W--> 286      (v) FRAGMENT TYPE:
287      (vi) ORIGINAL SOURCE:
289      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
291 CGGGATCCCA TATGCAGGTT TCTGATGTC CGCGTGACCT GGAAGTTGTT GCTGCGACC      59
293 (2) INFORMATION FOR SEQ ID NO: 14:
295      (i) SEQUENCE CHARACTERISTICS:
296          (A) LENGTH: 55 base pairs
297          (B) TYPE: nucleic acid
298          (C) STRANDEDNESS: single
299          (D) TOPOLOGY: linear
301      (ii) MOLECULE TYPE: cDNA
302      (iii) HYPOTHETICAL: NO
C--> 303      (iv) ANTI-SENSE: NO
W--> 304      (v) FRAGMENT TYPE:
305      (vi) ORIGINAL SOURCE:
307      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
309 TAACTGCAGG AGCATCCCAG CTGATCAGCA GGCTAGTCGG GGTCGCAGCA ACAAC      55
311 (2) INFORMATION FOR SEQ ID NO: 15:
313      (i) SEQUENCE CHARACTERISTICS:
314          (A) LENGTH: 51 base pairs
315          (B) TYPE: nucleic acid
316          (C) STRANDEDNESS: single
317          (D) TOPOLOGY: linear
319      (ii) MOLECULE TYPE: cDNA
320      (iii) HYPOTHETICAL: NO
C--> 321      (iv) ANTI-SENSE: NO
W--> 322      (v) FRAGMENT TYPE:
323      (vi) ORIGINAL SOURCE:
325      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
327 CTCCTGCAGT TACCGTGCGT TATTACCGTA TCACGTACGG TGAAACCGGT G      51
329 (2) INFORMATION FOR SEQ ID NO: 16:
331      (i) SEQUENCE CHARACTERISTICS:
332          (A) LENGTH: 39 base pairs
333          (B) TYPE: nucleic acid
334          (C) STRANDEDNESS: single

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VERIFICATION SUMMARY

DATE: 07/26/2001

PATENT APPLICATION: US/09/637,614

TIME: 09:58:45

Input Set : N:\Crif3\RULE60\09637614.txt

Output Set: N:\CRF3\07262001\I637614.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:55 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:74 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:95 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:114 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:133 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:152 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:171 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:190 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:209 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:228 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:247 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:266 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:285 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:286 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
L:303 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:304 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14
L:321 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:322 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15
L:339 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:340 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:357 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:358 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:375 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:376 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:393 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:394 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:411 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:412 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20
L:429 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:430 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:447 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:448 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:465 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:466 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:483 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:484 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:501 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:502 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:519 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:520 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:537 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:538 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:555 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:556 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28

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L:573 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:574 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:591 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:592 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:609 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:628 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:647 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:666 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:685 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:704 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:723 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:742 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:761 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:780 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:799 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:818 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:856 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:875 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:894 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1788 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=93
L:1825 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=95
L:1862 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=97
L:1899 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=99
L:1937 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=101
L:1974 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=103
L:2011 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=105
L:2048 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=107
L:2132 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=111